SEQUENCE LISTING

<110> Sheehan, John
Thomas, Daryl
Barrett, Wade

<120> Algorithms for selection of primer pairs

<130> 1011U1

<140> 10/042,406
<141> 2002-01-09

<150> 60/317,311
<151> 2001-09-05

<160> 2

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Human

<400> 1

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aaaaaaaaaa aatcaaaaaa tgaaggagga tcacttgagc tctggaggtt gaggctgcaa 480
tgagccatga ttgcaccatt gcactcttgc ctgggtgaca gagtgagacc ctgcctcaaa 540
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ataatcttat tctagcaaat aaggatgtta gaatgcagca tattaaaata ttacaaaagt 660
acaatactat gaaaaaatat ggcactcaac acagagcaga atggaaacta gaattgaaca 720
gaggaaagta ttttgaactc ctgagtgcag gataggtttt tttcaataga tggtattggg 780
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<210> 2
<211> 855
<212> DNA
<213> Human

<220>
<221> misc_feature
<222> (306)...(433)
<223> n = A,T,C or G

<221> misc_feature

<222> (444)...(607)
<223> n = A,T,C or G

<400> 2
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taaacnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
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